

GenCore version 4.5  
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OK protein - protein search, using sw model

Run on: January 7, 2002, 15:49:07 ; Search time 101.88 Seconds

(without alignments)  
41.123 Million cell updates/sec

Title: US-08-569-749-5

Perfect score: 307

Sequence: 1 CELYRMSTYSTFPAGVPSSE.....KVCRCGGLMDNMKLGDSP 55

BLOSUM62

Scoring table: Gapop 10.0, Capext 0.5

Searched: 219241 segs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

1: PIR\_68.4  
2: PIR2.4  
3: PIR3.4  
4: PIR4.4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	307	100.0	618	2	S68450 apoptos is inhibito
2	301	98.0	604	2	S68449 apoptos is inhibito
3	159	51.8	457	2	S69544 apoptos is inhibito
4	140	45.6	358	2	JC5964 apoptos is inhibito
5	132	43.0	268	2	T10304 inhibitor of apopt
6	125	40.7	268	2	A53989 apoptos is-inhibiti
7	125	40.7	1232	2	A53478 neuronal apoptos is
8	122	39.7	1447	2	T42628 neuronal apoptos is
9	119	38.8	208	2	T03183 probable apoptos is
10	117	38.1	298	3	JC7968 kidney inhibitor o
11	103.5	33.7	275	2	A45679 inhibitor of apopt
12	103	33.6	150	2	T28409 ORF MSV48 probabl
13	102	33.2	496	2	S68452 apoptos is inhibito
14	93	30.3	457	2	S69545 apoptos is inhibito
15	92	28.2	275	2	T10310 apoptos is inhibito
16	86.5	28.2	292	2	T41772 IAP1 orf127 - Bomby
17	83.5	27.2	286	2	D36828 orf13 protein - Au
18	82	26.7	155	2	T30489 apoptos is inhibito
19	72.5	23.6	997	2	T43523 cul17 protein - fi
20	71.5	23.3	4845	2	T31067 BIR repeat contain
21	65.5	21.3	234	2	T30427 probable apoptos is
22	61	19.9	329	2	T28403 ORF MSV42 probabl
23	60	19.5	1401	2	T117452 Werner syndrome pr
24	59.5	19.4	1401	2	T30247 Werner syndrome pr
25	59.5	19.4	337	2	T27615 hypothetical prote
26	58	19.2	733	2	T04070 hypothetical prote
27	58	18.9	288	2	B72272 iron-sulfur cluste
28	57.5	18.7	616	2	A55796 ecatin precursor -
29	57	18.6	187	2	F86029 3-methyladenine DN

30	57	18.6	707	2	T40070 origin recognition
31	57	18.6	1930	2	F86200 protein p12k11.17
32	56	18.2	249	2	H72858 apoptos is inhibito
33	55	17.9	249	2	T41814 IAP2 orf71 - Bomby
34	55	17.9	932	2	H66325 hypothetical prote
35	55	17.9	1432	2	T01075 polyprotein - lepa
36	54.5	17.8	155	2	T37471 apoptos is inhibito
37	54.5	17.8	410	2	T49266 hypothetical prote
38	54.5	17.8	516	2	S40968 hypothetical prote
39	54.5	17.8	954	2	S47109 hypothetical prote
40	54.5	17.8	1192	2	G70512 5-methyltetrahydro
41	53.5	17.6	201	2	B70618 hypothetical prote
42	53.5	17.4	923	2	S10968 cytolesin precurs
43	53.5	17.4	949	2	E71940 translation initia
44	53	17.3	355	2	B64445 polytetraoxin 4x2
45	52	16.9	264	2	PC7035 cell division prot

#### ALIGNMENTS

RESULT 1  
S68450 apoptos is inhibitor hlap-2 - human  
C:Species: Homo sapiens (man)  
C>Date: 17-Jul-1998 #sequence\_rev1sion 17-Jul-1998 #text\_change 21-Jul-2000  
C:Accession: S68450  
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Faraha  
Nature 379, 349-353, 1996  
A>Title: Suppression of apoptos is in mammalian cells by NAIP and a related family of  
A:Reference number: A50182; MUID:96149249  
A:Accession: S68450  
A>Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-618 <LIS>  
A:Cross references: EMBL:U45879; NID:q1184317; PTDN:AAC50372.1; PTD:q1184318  
C:Function:  
A:Description: apoptotic suppressor  
C:Superfamily: RING finger homology  
C:Keywords: apoptos is; zinc finger  
F:567-611/Domain: RING finger homology <RNG>

Query Match 100.0%; Score 307; DB 2; Length 618;  
Best Local Similarity 100.0%; Pred. No. 1.6e-31;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CELYRMSTYSTFPAGVPSSESLARAGFYVTGVNDVKFCGCCGLMDNMKLGDSP 55  
Db 45 CELYRMSTYSTFPAGVPSSESLARAGFYVTGVNDVKFCGCCGLMDNMKLGDSP 99

RESULT 2  
S68449 apoptos is inhibitor hlap-1 - human  
C:Species: Homo sapiens (man)  
C>Date: 17-Jul-1998 #sequence\_rev1sion 17-Jul-1998 #text\_change 21-Jul-2000  
C:Accession: S68449  
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Faraha  
Nature 379, 349-353, 1996  
A>Title: Suppression of apoptos is in mammalian cells by NAIP and a related family of  
A:Reference number: A50182; MUID:96149249  
A:Accession: S68449  
A>Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-604 <LIS>  
A:Cross references: EMBL:U45879; NID:q1184315; PTDN:AAC50371.1; PTD:q1184316  
C:Function:  
A:Description: apoptotic suppressor  
C:Superfamily: RING finger homology  
C:Keywords: apoptos is; zinc finger  
F:553-597/Domain: RING finger homology <RNG>

[illegible]

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Matches      25      Conservative      6;      Mismatches      20;      Indels      0;      Gaps      0;

Oy      5      RMSTYSTPAGVPSRSLSARAGPYTGYGNKVCRCGCGMLDMKWLGDSP      55
      | : : : : | | | | | | | | | | | | | | | | | | | | |
Db      99      RPKTKCMWPSSTPYHREQVLASGFTYGHSDVDVCFCCDGGLRWESGDDP      143

RESULT      5
T10304
Inhibitor of apoptosis protein 3 - Orygia pseudotsugata nuclear polyhedrosis virus
C:Species: Orygia pseudotsugata nuclear polyhedrosis virus, OPMNV
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Sep-2000
C:Accession: T10304
R:Altmann, G.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohmann, G.F.
Virology 229, 381-399, 1997
I:Title: The sequence of the Orygia pseudotsugata multinnucleocapsid nuclear polyhedro
A:Reference number: Z17011; MUID:97271300
A:Accession: T10304
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-268 <ABR>
C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology
F:217-261/Domain: RING finger homology <RRN>

Query Match      43.0%;      Score 132;      DB 2;      Length 268;
Best Local Similarity 42.6%;      Pred. No. 2, 2e-09;
Matches 23;      Conservative 10;      Mismatches 21;      Indels 0;      Gaps 0;

Oy      2      ELYMSTVSTPAGVPSRSLSIARAGPYTGYGNKVCRCGCGMLDMKWLGDSP      55
      | : : : : | | | | | | | | | | | | | | | | | | | | |
Db      111      EAAULTFAEMPRGLAKQREBLASAGFTYGGSKTRFCDCDGLAKMPDPADP      164

RESULT      6
Apostosis-inhibiting protein - Orygia pseudotsugata multicapsid nuclear polyhedrosis
C:Species: Orygia pseudotsugata multicapsid nuclear polyhedrosis virus, OPMNV
C:Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 15-Sep-2000
C:Accession: A53989
R:Birnbaum, M.J.; Clum, R.J.; Miller, L.K.
J. Virol. 68, 2521-2528, 1994
A:Title: An apoptosis-inhibiting gene from a nuclear polyhedrosis virus encoding a po
A:Reference number: A53989; MUID:94187094
A:Accession: A53989
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-266 <ABR>
C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology
F:217-261/Domain: RING finger homology <RRN>

Query Match      43.0%;      Score 132;      DB 2;      Length 268;
Best Local Similarity 42.6%;      Pred. No. 2, 2e-09;
Matches 23;      Conservative 10;      Mismatches 21;      Indels 0;      Gaps 0;

Oy      2      ELYMSTVSTPAGVPSRSLSIARAGPYTGYGNKVCRCGCGMLDMKWLGDSP      55
      | : : : : | | | | | | | | | | | | | | | | | | | | |
Db      111      EAAULTFAEMPRGLAKQREBLASAGFTYGGSKTRFCDCDGLAKMPDPADP      164

RESULT      7
neutonal apoptosis inhibitory protein - human
A:Accession: A53478
A:Title: apoptosis inhibitory protein - human
A:Molecule type: N/AIP
C:Species: Homo sapiens (man)
C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 02-Feb-2001
C:Accession: A53478
R:Koy, N.; Mahadevan, M.S.; McLean, M.; Shuler, G.; Varugh, Z.; Parahani, R.; Balder
d, T.O.; de Jong, F.J.; Suth, L.; Ikeda, J.E.; Korneluk, R.G.; Mackenzie, A.

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Cell80_167-178_1995
A:Title: The gene for neuronal apoptosis inhibitory protein is partially deleted in Ind
A:Reference number: A55478; MUID:95112344
A:Accession: A55478
A:Molecule type: mRNA
A:Residues: 1-1232 <ROR>
A:Cross-references: GB-U19251
C:Genetics:
A:Gene: GDB:SMA@ SMA
A:Cross-references: GDB:120378; OMIM:600354; OMIM:253300
A:Map position: 5q12.2-5q13
C:Keywords: apoptosis; ATP; glycoprotein; nucleotide binding; P-loop; transmembrane prote
F:54-110/Domin: transmembrane-binding motif A (P-loop)
F:4470-477/Region: nucleotide-binding site predicted <TM1>
F:479-496/Domain: transmembrane *status predicted <TM2>
F:479-496/Domain: transmembrane *status predicted
F:618-632,823,923,1035/Binding site: carbohydrate (Asn) (covalent) *status predicted

Query Match          40.7%; Score 125; DB 2; Length 1232;
Best Local Similarity 40.7%; Pred. No. 7, 5e-08;
Matches 22; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

Oy      2 ELYRRSTYTFPGAPVYSERSIARAGGYTYGNKVKACCGCLMDNKLMDSPF 55
        | : : : : | : : : : | : : : : | : : : : | : : : : |
Db      278 ELRLDPSFKDWPRISAVGVALAKKGFLTGTIKDIYQCSFGCCLEWNGEDDP 331

RESULT      8
T42628
neural apoptosis inhibitory protein 2 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
C:Accession: T42628
R:Yangshl Z.; Diez E.; Gros P.; Mackenzie A.
A>Title: cDNA cloning and the 5'genomic organization of Malp2, a candidate gene for murin
A:Reference number: J221179; MUID:99315342
A:Accession: T42628
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1447 <XAR>
A:Cross-references: EMBL:AF102871; NID:g3606228; PID:g3606229; PID:NAC73002.1
C:Genetics:
A:Gene: Malp2

Query Match          39.7%; Score 122; DB 2; Length 1447;
Best Local Similarity 40.7%; Pred. No. 2, 1e-07;
Matches 22; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

Oy      2 ELYRRSTYTFPGAPVYSERSIARAGGYTYGNKVKACCGCLMDNKLMDSPF 55
        | : : : : | : : : : | : : : : | : : : : | : : : : |
Db      278 ELRLDPSFKDWPRISAVGVALAKKGFLTGTIKDIYQCSFGCCLEWNGEDDP 331

RESULT      9
T03183
probable apoptosis inhibitor - Chilo iridescent virus
A:Species: Chilo iridescent virus
C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 02-Sep-2000
C:Accession: T03183
R:Bahr U.; Yltona C.A.; Darai G.
A>Title: The DNA sequence of Chilo iridescent virus between the genome coordinates 0..101
A:Reference number: Z14834; MUID:96141693
A:Accession: T03183
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-208 <BAH>
A:Cross-references: EMBL:AF003534; NID:g2738385; PID:NAB94481.1; PID:g2738454
C:Superfamily: RING finger homology
C:Subfamily: RING finger homology <RRN>
C:Subfamily: RING finger homology <RRN>

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QY      5 RNSSTVTFPAGVPYSERSLARAGYYGVNOKVCACCGCLTMDMKLDDSP   55  
       10 : : : : | : ||| : : :||| : : :||| : : :|||  
Db     40 RLMSFQMNPQLCPKESGLSRAGFYLTGNIGDVGCFCDJAKMRKSNDP    90  
  
RESULT 10  
JC7568  
Kidney Inhibitor of apoptosis protein - human  
C.Species: Homo sapiens (man)  
C.Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 31-Mar-2001  
C.Accession: JG7568  
R.Lin.: J.H.; Deng., G.; Huang, O.; Morser, J.  
Biochem. Biophys. Res. Commun. 279, 820-831, 2000  
A.Title: KIAA, a novel member of the inhibitor of apoptosis protein family.  
A.Reference number: JC7568; MUID: 21092523  
A.Contents: Fetal kidney  
A.Accession: JC7568  
A.Molecule type: mRNA  
A.Residues: 1-298 <lin>  
C.Comment: This protein, a new member of the inhibitor of apoptosis protein family,  
C.Genetics:  
A.Gene: KIAA  
A.Map position: 20q13.3  
C.Keywords: apoptosis
```

```
Query Match           38.1%; Score 117; DB 3; Length 298;  
Best Local Similarity 42.6%; Pred. No. 2, le=07;  
Matches 23; Conservative 9; Mismatches 22; Indels 0; Gaps 0;
```

```
OY      2 ELYRMSTVFPAQPVPSERSLARAGYGTGYNDXKCPCGCCGLTMIDNKLLDSP   55  
       10 : : : : | : ||| : : :||| : : :||| : : :|||  
DB     97 ELRLASTVDNELTEVPBLIAAGAFTGHQQVKCPFCTSGLSDMKKGDPE   140  
  
RESULT 11  
A45679  
Inhibitor-of-apoptosis polypeptide (IAP) - Cydia pomonella granulosis virus CpGV  
C.Species: Cydia pomonella granulosis virus Cpvv  
C.Date: 21-Sep-1993 #sequence_revision 23-Apr-1997 #text_change 15-Sep-2000  
C.Accession: A45679  
R.Crook, N.E.; Clem, R.J.; Miller, L.K.  
J. Virol. 67, 2168-2174, 1993  
A>Title: An apoptotic-inhibiting baculovirus gene with a zinc finger-like motif.  
A.Reference number: A45679; MUID:931B1E8  
A.Accession: A45679  
A.Status: preliminary  
A.Molecule type: DNA  
A.Residues: 1-275 <cdo>  
A.Note: sequence extracted from NCBI backbone (NCBIT:127014, NCBIT:127015)  
C:Superfamily: viral apoptotic inhibitor IAP; RING finger homology
```

```
Query Match          33.7%; Score 103.5; DB 2; Length 275;  
Best Local Similarity 35.2%; Pred. NO. 1e=05;  
Matches 19; Conservative 14; Mismatches 20; Indels 1; Gaps 1;
```

```
OY      2 ELYRMSTVFPAQPVPSERSLARAGYGTGYNDXKCPCGCCGLTMIDNKLLDSP   55  
       10 : : : : | : ||| : : :||| : : :||| : : :|||  
DB     7 EEVRILNTFEKMVSF-LSEPMAKNKGTYLGSDSVCAFCVEIMIRWKKEGEDE   59  
  
RESULT 12  
T28409  
rRE MSV448 probable inhibitor of apoptosis protein (IAP) - Melanoplus sanguinalipes entomobryon
```

C:Species: Melanoplus sanguinipes entomopoxvirus  
C>Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jul-2000  
C/Accession: T28409  
R/Mfonso, C.L.; Tulman, E.R.; Lu, Z.; Oms, E.; Kulsch, G.F.; Rock, D.L.  
J. Virol. 73, 533-552, 1999  
A>Title: The genome of Melanoplus sanguinipes entomopoxvirus.  
A/Reference number: 220484; PMID:9105612  
A/Accession: T28409  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-150 <AF0>  
A:Cross-references: EMBL:AF063866; NID:g4049647; PIDN:AAC97724.1; PID:g4049764  
C/Genetic?:  
A>Note: MSV248

Query Match                33.6%    Score 103; DB 2; Length 150;  
Best Local Similarity     33.3%;    Pred: Msc. 6.7e-05;  
Matches 18; Conservative    9; Mis.Matches 24; Indels      0; Gaps      0;

OY            5 RASTYSTPACGVPSERSLARAGFYITGCYNDRKACPCCGCLMDNMKLGDSP 55  
             ::::~::~:~::~::~::~::~::~::~::~::~::~::~::~::~::~::~:  
db          19 RIISSENNPIISLEPKINIKRCAGGYTNTIGIITCCNGGLINKMLKIPLYNDP 69

RESULT 13  
S68452  
apoptosis inhibitor dlap - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 17-Nov-2000  
C:Accession: S68452; S78528  
R:Liston, P.; Roy, N.; Tamal, K.; LeFebvre, C.; Bald, S.; Chertton-Horvat, G.; Farahani,  
Nature 379, 349-355, 1996  
A>Title: Suppression of apoptosis in mammalian cells by NATp and a related family of IAH  
A:Reference number: A58182; MIMD:96149249  
A:Accession: S68452  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-496 <LTS>  
A:Cross-references: EMBL:U05081; MID:g1104313; PIDN:AMC46988.1; PID:g1104314  
R:Bald, S.D.  
submitted to the EMBL Data Library, January 1996  
A:Reference number: S78528  
A:Accession: S78528  
A:Molecule type: mRNA  
A:Residues: 1-36, AT, 3', 'K', 39, 'L', 41-44, 'H', 46-58, 'Q', 60-61, 'N', 61-62, 'A', 63-64, 'A', 65-66, 'A', 67-68, 'A', 69-70, 'A', 71-72, 'A', 73-74, 'A', 75-76, 'A', 77-78, 'A', 79-80, 'A', 81-82, 'A', 83-84, 'A', 85-86, 'A', 87-88, 'A', 89-90, 'A', 91-92, 'A', 93-94, 'A', 95-96, 'A', 97-98, 'A', 99-100, 'A', 101-102, 'A', 103-104, 'A', 105-106, 'A', 107-108, 'A', 109-110, 'A', 111-112, 'A', 113-114, 'A', 115-116, 'A', 117-118, 'A', 119-120, 'A', 121-122, 'A', 123-124, 'A', 125-126, 'A', 127-128, 'A', 129-130, 'A', 131-132, 'A', 133-134, 'A', 135-136, 'A', 137-138, 'A', 139-140, 'A', 141-142, 'A', 143-144, 'A', 145-146, 'A', 147-148, 'A', 149-150, 'A', 151-152, 'A', 153-154, 'A', 155-156, 'A', 157-158, 'A', 159-160, 'A', 161-162, 'A', 163-164, 'A', 165-166, 'A', 167-168, 'A', 169-170, 'A', 171-172, 'A', 173-174, 'A', 175-176, 'A', 177-178, 'A', 179-180, 'A', 181-182, 'A', 183-184, 'A', 185-186, 'A', 187-188, 'A', 189-190, 'A', 191-192, 'A', 193-194, 'A', 195-196, 'A', 197-198, 'A', 199-200, 'A', 201-202, 'A', 203-204, 'A', 205-206, 'A', 207-208, 'A', 209-210, 'A', 211-212, 'A', 213-214, 'A', 215-216, 'A', 217-218, 'A', 219-220, 'A', 221-222, 'A', 223-224, 'A', 225-226, 'A', 227-228, 'A', 229-230, 'A', 231-232, 'A', 233-234, 'A', 235-236, 'A', 237-238, 'A', 239-240, 'A', 241-242, 'A', 243-244, 'A', 245-246, 'A', 247-248, 'A', 249-250, 'A', 251-252, 'A', 253-254, 'A', 255-256, 'A', 257-258, 'A', 259-260, 'A', 261-262, 'A', 263-264, 'A', 265-266, 'A', 267-268, 'A', 269-270, 'A', 271-272, 'A', 273-274, 'A', 275-276, 'A', 277-278, 'A', 279-280, 'A', 281-282, 'A', 283-284, 'A', 285-286, 'A', 287-288, 'A', 289-290, 'A', 291-292, 'A', 293-294, 'A', 295-296, 'A', 297-298, 'A', 299-300, 'A', 301-302, 'A', 303-304, 'A', 305-306, 'A', 307-308, 'A', 309-310, 'A', 311-312, 'A', 313-314, 'A', 315-316, 'A', 317-318, 'A', 319-320, 'A', 321-322, 'A', 323-324, 'A', 325-326, 'A', 327-328, 'A', 329-330, 'A', 331-332, 'A', 333-334, 'A', 335-336, 'A', 337-338, 'A', 339-340, 'A', 341-342, 'A', 343-344, 'A', 345-346, 'A', 347-348, 'A', 349-350, 'A', 351-352, 'A', 353-354, 'A', 355-356, 'A', 357-358, 'A', 359-360, 'A', 361-362, 'A', 363-364, 'A', 365-366, 'A', 367-368, 'A', 369-370, 'A', 371-372, 'A', 373-374, 'A', 375-376, 'A', 377-378, 'A', 379-380, 'A', 381-382, 'A', 383-384, 'A', 385-386, 'A', 387-388, 'A', 389-390, 'A', 391-392, 'A', 393-394, 'A', 395-396, 'A', 397-398, 'A', 399-400, 'A', 401-402, 'A', 403-404, 'A', 405-406, 'A', 407-408, 'A', 409-410, 'A', 411-412, 'A', 413-414, 'A', 415-416, 'A', 417-418, 'A', 419-420, 'A', 421-422, 'A', 423-424, 'A', 425-426, 'A', 427-428, 'A', 429-430, 'A', 431-432, 'A', 433-434, 'A', 435-436, 'A', 437-438, 'A', 439-440, 'A', 441-442, 'A', 443-444, 'A', 445-446, 'A', 447-448, 'A', 449-450, 'A', 451-452, 'A', 453-454, 'A', 455-456, 'A', 457-458, 'A', 459-460, 'A', 461-462, 'A', 463-464, 'A', 465-466, 'A', 467-468, 'A', 469-470, 'A', 471-472, 'A', 473-474, 'A', 475-476, 'A', 477-478, 'A', 479-480, 'A', 481-482, 'A', 483-484, 'A', 485-486, 'A', 487-488, 'A', 489-490, 'A', 491-492, 'A', 493-494, 'A', 495-496, 'A', 497-498, 'A', 499-500, 'A', 501-502, 'A', 503-504, 'A', 505-506, 'A', 507-508, 'A', 509-510, 'A', 511-512, 'A', 513-514, 'A', 515-516, 'A', 517-518, 'A', 519-520, 'A', 521-522, 'A', 523-524, 'A', 525-526, 'A', 527-528, 'A', 529-530, 'A', 531-532, 'A', 533-534, 'A', 535-536, 'A', 537-538, 'A', 539-540, 'A', 541-542, 'A', 543-544, 'A', 545-546, 'A', 547-548, 'A', 549-550, 'A', 551-552, 'A', 553-554, 'A', 555-556, 'A', 557-558, 'A', 559-560, 'A', 561-562, 'A', 563-564, 'A', 565-566, 'A', 567-568, 'A', 569-570, 'A', 571-572, 'A', 573-574, 'A', 575-576, 'A', 577-578, 'A', 579-580, 'A', 581-582, 'A', 583-584, 'A', 585-586, 'A', 587-588, 'A', 589-590, 'A', 591-592, 'A', 593-594, 'A', 595-596, 'A', 597-598, 'A', 599-600, 'A', 601-602, 'A', 603-604, 'A', 605-606, 'A', 607-608, 'A', 609-610, 'A', 611-612, 'A', 613-614, 'A', 615-616, 'A', 617-618, 'A', 619-620, 'A', 621-622, 'A', 623-624, 'A', 625-626, 'A', 627-628, 'A', 629-630, 'A', 631-632, 'A', 633-634, 'A', 635-636, 'A', 637-638, 'A', 639-640, 'A', 641-642, 'A', 643-644, 'A', 645-646, 'A', 647-648, 'A', 649-650, 'A', 651-652, 'A', 653-654, 'A', 655-656, 'A', 657-658, 'A', 659-660, 'A', 661-662, 'A', 663-664, 'A', 665-666, 'A', 667-668, 'A', 669-670, 'A', 671-672, 'A', 673-674, 'A', 675-676

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Query Match          33.2% Score 102: DB 2: Length 496:
Best Local Similarity 34.5% Pred. No. 2.8e-05:
Matches 19; Conservative 12; Mismatches 24; Indels 0; Gaps 0;

OY      1  CELYRSTYSFPGAGVPSERSLARAGFYGYVNDKVKYCCGGLMLNNKLLDSP 55
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      209  CVBARLRPFDTWPISTINQPSALNAGLGYCKIDQYRGFRHGNGLNSNQKEDER 263

RESULT 14
S69345
apoptosis inhibitor IAP homolog - fruit fly (Drosophila melanogaster)
C/Species: Drosophila melanogaster
C/Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C/Accession: S69345
R/Buckett, C.S.; Nave, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Gillfillan, M.C.
EMBO J. 15, 2685-2694, 1996

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A:Title: A conserved family of cellular genes related to the baculovirus iap gene and  
A:Reference number: S69544; MUID:96256286  
A:Accession: S69545  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-497 <DNC>  
A:Cross-references: EMBL:U03273; NID:g1019116; PIDD:AMC4155.1; PID:g1019117  
C:Genotols:  
A:Gene: I1p  
C:Superfamily: apoptosis inhibitor IAP homolog; RING finger homology  
E:446-450/Domain: RING finger homology <RNF>

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Query Match      33.2%, Score 102; DB 2; Length 497;
Best Local Similarity 34.5%; Pred. No. 2.8e-05;
Matches 19; Conservative 12; Mismatches 24; Indels 0; Gaps 0;

Oy      1 CELRRSTYSYTFPGAGVPSERSLARKGAPFYTGVDNKCCFCGCCMLDNNKLGDSP 55
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Db      211 CVDARLRRTFTDMPISNIDPASAALQAGLYYOKIGDVRCFRHCIONGLRSMQKEDEP 265

RESULT 15
T10310
apoptosis-inhibiting protein 1 - Orygia pseudotsugata nuclear polyhedrosis virus
C:Species: Orygia pseudotsugata nuclear polyhedrosis virus, OPMPV
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Sep-2000
C:Accession: T10310
R:Afrans, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F.
Virology 229, 381-399, 1997
A>Title: The sequence of the Orygia pseudotsugata multinucleocaptod nuclear polyhedro-
A:Reference number: Z17011; MWID: 97271300
A:Accession: T10310
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-275 <AHR>
A:Cross-references: EMBL:U75930; NID:g2934903; PTDN:AAC59040.1; PID:g1911287
C:Superfamily: Viral apoptosis inhibitor IAP; RING finger homology <RNS>
?;223-266/Domain: RING finger homology <RNS>
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Query Match 30.38; Score 93; DB 2; Length 275;  
Best Local Similarity 31.4%; Pred. No. 0.00023;  
Matches 16; Conservative 11; Mismatches 24; Indels 0; Gaps 0-;

OY 5 RMSTSTTPACGYPSRSLAAGAYTGTGYNKKCCGLMLDMKALGSP 55  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db 129 RRATFDHMPAAALNLTHDIALDAQGFPTMLGSGETCEFCDCIKVRMLRGSDP 179

Search completed: January 7, 2002, 15:49:08  
Job time: 702 sec



